

[illegible]

4. US-09-508-832-2 (1-110)
US-09-508-832-8 Sequence 8, Application US/09508832

Initial Score	=	63	Optimized Score	=	94	Significance	=	1.28
Residue Identity	=	63%	Matches	=	87	Mismatches	=	21
Gaps	=	28	Conservative Substitutions	=	2			

X 10 20 30 40
MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLSQTEPQASIRQS-----
|||||
MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLSQTEPQASIRQS
X 10 20 30 40 50 60 70
MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLSQTEPQDRSPAPMSCKDKSTQTSPPCQAFNHLYLSAMA

```

      50    60    70    80    90   100   110
---QEEPELPEIRIAQLRRIGDEFNTYTRRVFANDYREADHPQMVLGLLRIFRLVWRH
      | | : ||| ||||| ||| | | | | | | | | | | | | | | | | |
SMROAEPADMREPETIAQLRRIGDEFNAYRFRVFNLYNQAAEDPRMVLRLRLRYIVRLVWRH
      80    90   100   110   120   130

```

5. US-09-508-832-2 (1-110)
US-09-508-832-10 Sequence 10, Application US/09508832

Initial Score	=	61	Optimized Score	=	69	Significance	=	1.21
Residue Identity	=	35%	Matches	=	48	Mismatches	=	58
Gaps	=	26	Conservative Substitutions	=	4			

[illegible]

-----RRIGDFENETTYRRVANDYREADEHPQWILQLLRIFRFLVWRHRH 70 80 90 100 110

FATRSPLEIFMRSSLLSRSSGYSFEDTDRSPAPMSCDKSTQTFPPCQAFNHVLSAMASHRQ 80 90 100 110 120 130 X

EWIAQELRRIGDEFNAYYARRVFLNNYQAAEDHPRMVILRL
150 160 170 180

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4
Results file Seq4-Peptides.res made by tport on Thu 10 Jul 103 11:30:19-PDT.
Query sequence being compared:US-09-508-832-4 (1-140)
Number of sequences searched: 21
Number of scores above cutoff: 21
Results of the initial comparison of US-09-508-832-4 (1-140) with:
File : US09508832.pep

100-
-
N -
U 50-
M -
B -
E -
R -
O -
F 10-
-
S -
E 5- **
Q -
U -
E -
N -
C -
E - **
S 0-
SCORE 0 116 31 47 62 78 93 109 124 140
STDEV 0
PARAMETERS
Similarity matrix PAM-150 K-tuple 1
Threshold level of sim. 16%
Mismatch penalty 1 Joining penalty 20
Gap penalty 5.00 Window size 110
Gap size penalty 0.05
Cutoff score 2
Randomization group 0
SEARCH STATISTICS
Scores: Mean Median Standard Deviation
30 11 39.47
Times: CPU
00:00:00.00 Total Elapsed
00:00:00.00
Number of residues: 1041
Number of sequences searched: 21
Number of scores above cutoff: 21

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was found:
Sequence Name Description Init. Opt. Length Score Score Sig. Frame

1. US-09-508-832-4 Sequence 4, Application US 140 140 140 2.79 0
The list of other best scores is:
Sequence Name Description Length Score Score Init. Opt. Frame

2. US-09-508-832-6 Sequence 6, Application US 196 99 118 1.75 0
3. US-09-508-832-8 Sequence 8, Application US 138 92 126 1.57 0
4. US-09-508-832-10 Sequence 10, Application US 198 78 82 1.22 0
5. US-09-508-832-2 Sequence 2, Application US 110 69 105 0.99 0
1. US-09-508-832-4 (1-140)
US-09-508-832-4 Sequence 4, Application US/09508832
Initial Score = 140 Optimized Score = 140 Significance = 2.79
Residue Identity = 100% Matches = 140 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0
X 10 20 30 40 50 60 70
MAKQPSDVSECDREGGQLOPAERPPQLRPGAPTSLOTPEQDRSPAPMSCDKSTQTPSPCOAFNHYLSAMA
|||||
MAKQPSDVSECDREGGQLOPAERPPQLRPGAPTSLOTPEQDRSPAPMSCDKSTQTPSPCOAFNHYLSAMA
X 10 20 30 40 50 60 70
80 90 100 110 120 130 140 X
SIRSQEPEPDLRPEIRIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRHH
|||||
SIRSQEPEPDLRPEIRIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRHH
80 90 100 110 120 130 140
2. US-09-508-832-4 (1-140)
US-09-508-832-6 Sequence 6, Application US/09508832
Initial Score = 99 Optimized Score = 118 Significance = 1.75
Residue Identity = 73% Matches = 103 Mismatches = 35
Gaps = 0 Conservative Substitutions = 2
X 10 20 30 40 50 60 70
DVSSECDREGGQLOPAERPPQLRPGAPTSLOTPEQGNPDGCDRCPHSGPGLAPSPGPPATSPLEFIF
10 20 30 40 50 60 70
30 40 50 60 70 80 90
ERPPQLRPGAPTSLOTPEQDRSPAPMSCDKSTQTPSPCOAFNHYLSAMASIRSQEPEPDLRPEIRIAQEL
|||||
VRRSLLSRSSGYSFSDTDRSPAPMSCDKSTQTPSPCOAFNHYLSAMASIRSQEPEPDLRPEIRIAQEL
80 90 100 110 120 130 140 150
100 110 120 130 140
RRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRHH
|||||
RRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRHH
160 170 180 190 X
3. US-09-508-832-4 (1-140)
US-09-508-832-8 Sequence 8, Application US/09508832
Initial Score = 92 Optimized Score = 126 Significance = 1.57
Residue Identity = 85% Matches = 120 Mismatches = 15
Gaps = 2 Conservative Substitutions = 3
X 10 20 30 40 50 60 70
MAKQPSDVSECDREGGQLOPAERPPQLRPGAPTSLOTPEQDRSPAPMSCDKSTQTPSPCOAFNHYLSAMA
|||||
MAKQPSDVSECDREGGQLOPAERPPQLRPGAPTSLOTPEQDRSPAPMSCDKSTQTPSPCOAFNHYLSAMA

```
X      10      20      30      40      50      60      70
      80      90     100     110     120     130     140
SIROSEPEDLRPEIRIAQELRIGDEFNETHYRRVFANDYREAEHPQMWILQLLRFIFRLVWRRH
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
SMRQA--EPADMREIPIAQLRIGDEFNETHYRRVFANDYREAEHPQMWILQLLRFIFRLVWRRH
      80      90     100     110     120     130     140
X
```

```
4. US-09-508-832-4 (1-140)
US-09-508-832-10 Sequence 10, Application US/09508832

Initial Score = 78 Optimized Score = 82 Significance = 1.22
Residue Identity = 32% Matches = 53 Mismatches = 82
Gaps = 23 Conservative Substitutions = 5

X      10      20      30      40      50      60      70
MAKOPSDVSECDEGREGQLQPAERPPOLRPGAPTSLOTPEODRSPAPMSCDKSTQTPTSPPCQAFNHYLSAMA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
MAKOPSDVSECDEGREGQLQPAERPPOLRPGAPTSLOTPEODRSPAPMSCDKSTQTPTSPPCQAFNHYLSAMA
X      10      20      30      40      50      60      70
SIROSQ-----EEPEDLRPEIRIAQELRIGDEFNETHYRRVFANDYREAEHP
FATRSPLFIPIRRSSLSRSSGYSFSDTDRSPAPMSCDKSTQTPTSPPCQAFNHYLSAMASMRQAEPADMRP
      80      90     100     110     120     130     140
OMVILQLLRFIFRLVWRRH
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
EIIIAQELRIGDEFNETHYRRVFANDYREAEHPQMWILQLLRFIFRLVWRRH
      150     160     170     180     190
```

```
5. US-09-508-832-4 (1-140)
US-09-508-832-2 Sequence 2, Application US/09508832

Initial Score = 69 Optimized Score = 105 Significance = 0.99
Residue Identity = 78% Matches = 110 Mismatches = 0
Gaps = 30 Conservative Substitutions = 0

X      10      20      30      40      50      60      70
MAKOPSDVSECDEGREGQLQPAERPPOLRPGAPTSLOTPEODRSPAPMSCDKSTQTPTSPPCQAFNHYLSAMA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
MAKOPSDVSECDEGREGQLQPAERPPOLRPGAPTSLOTPEODRSPAPMSCDKSTQTPTSPPCQAFNHYLSAMA
X      10      20      30      40      50      60      70
SIROSEPEDLRPEIRIAQELRIGDEFNETHYRRVFANDYREAEHPQMWILQLLRFIFRLVWRRH
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
SIROSEPEDLRPEIRIAQELRIGDEFNETHYRRVFANDYREAEHPQMWILQLLRFIFRLVWRRH
      50      60      70      80      90     100     110
```

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FastDB - Fast Pairwise Comparison of Sequences Release 5.4

Results file Seq6-peptides.res made by tport on Thu 10 Jul 103 11:31:54-PDT.

Query sequence being compared: US-09-508-832-6 (1-196)
 Number of sequences searched: 21
 Number of scores above cutoff: 21

Results of the initial comparison of US-09-508-832-6 (1-196) with:
File : US09508832.pep

[illegible]

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Init. Opt.	Length	Score	Sig.	Frame
.						

1. US-09-508-832-6 Sequence 6, Application US 196 196 196 3.30 0

The list of other best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Sig. Frame
*** 1 standard deviation above mean ***					
2. US-09-508-832-10	Sequence 10, Application	198	112	177	1.60 0
3. US-09-508-832-4	Sequence 4, Application US	140	98	117	1.32 0
*** 0 standard deviation from mean ***					
4. US-09-508-832-8	Sequence 8, Application US	138	75	79	0.85 0
5. US-09-508-832-2	Sequence 2, Application US	110	69	85	0.73 0
1. US-09-508-832-6 (1-196)					
US-09-508-832-6 Sequence 6, Application US/09508832					
Initial Score	=	196	Optimized Score	=	196
Residue Identity	=	100%	Matches	=	196
Gaps	=	0	Conservative Substitutions	=	0
		Significance		=	3.30
		Mismatches		=	0
				=	0

	10	20	30	40	50	60	70
X	MAKQSDVSECDREGQLOPAERPOLRGAPTSLQTEPQGNPDGDCRPHGSGOGPLAPASPGPFATR						
	MAKQSDVSECDREGQLOPAERPOLRGAPTSLQTEPQGNPDGDCRPHGSGOGPLAPASPGPFATR						
X	MAKQSDVSECDREGQLOPAERPOLRGAPTSLQTEPQGNPDGDCRPHGSGOGPLAPASPGPFATR						
	X	10	20	30	40	50	60
	80	90	100	110	120	130	140
	SPLFIEVRSSLLSRSSGYFSDTORSPAPMSCDKSTQTPPPCOAFNHYLSAMASIROSQEEDLRLPEI						
	SPLFIEVRSSLLSRSSGYFSDTORSPAPMSCDKSTQTPPPCOAFNHYLSAMASIROSQEEDLRLPEI						
	X	80	90	100	110	120	130
	140						

2. US-09-508-832-6 (1-196)
US-09-508-832-10 Sequence 10, Application US/09508832

[illegible]

3. US-09-508-832-6 (1-196)
US-09-508-832-4 Sequence 4, Application US/09508832

```
Initial score = 98 .Optimized score = 117 Significance = 1.32
Residue Identity = 73% Matches = 103 Mismatches = 35
```


IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file Seg1-Nucs.res made by tport on Thu 10 Jul 103 11:35:13-PDT.

Query sequence being compared:US-09-508-832-1 (1-332)
 Number of sequences searched: 18
 Number of scores above cutoff: 18

Results of the initial comparison of US-09-508-832-1 (1-332) with:
File : US09508832.seq

[illegible]

TATTTTGAATAATTACCAAGCAGCCGGAAGACCAACCCACGAATGGTTATCTTACGACTGTTACGTTACATTG
500 510 520 530 540 550 560 570
310 320 330 X
TCCGCTCTGGTATGGAGAGGCATTG
||||| ||||| ||||| |||||
TCCGCTGGTGTGGAGAAATGCATTG
580 590 X

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CTCTCCAGCTCAGGCTGGGGCCCTAGCTCCCTACAGACAAACCGCAAGACAGAGCGCGGACCCCATG
150 160 170 180 190 200 210
AGTTGTGACAAGTCAACACAAACCCCAAGTCCCTTGGCAGGCTTCAACCACTATCTCAGTGCATGGCT
|||||
CTCTCCAGCTCAGAGCTGGGGCCCTAGCTCCCTACAGACAGAGCCCAAGACAGAGCGCGGACCCCATG
150 160 170 180 190 200 210
AGTTGTGACAAGTCAACACAAACCCCAAGTCCCTTGGCAGGCTTCAACCACTATCTCAGTGCATGGCT
150 160 170 180 190 200 210
220 230 240 250 260 270 280
TCCATACGACGCTCTCAGGAGCAACTGAAGATCTGCGCCGAGATACGATTCACAGAGCTGGCGGG
|||||
TCCATGAGGAGCT-----GAACCTGAGATATCGCCAGAGATATGGATCGGCCAAGAGTTGGCGGT
220 230 240 250 260 270 280
290 300 310 320 330 340 350
ATCGGAGAGGTTCAACGAAACTTACACAAGAGGCTGTTTGAATGATTACCGCGAGGCTGAAGACCA
|||||
ATCGGAGAGGTTTAACTTACTATGCAAGGAGGATTTTGAATATATACCAAGCAGCGGAAGACCAC
290 300 310 320 330 340 350
370 380 390 400 410 420 X
CTCTAAATGGTTATCTTACAACGTTTACGCTTTATCTCCGCTGTGTATGAGAGGCAATG
|||||
CCACGAATGGTTATCTTACGCTTACGTTTACATTTGCTCGGCTGTGGAGAAATGCAATG
360 370 380 390 400 410 X
```

3. US-09-508-832-3 (1-422)
US-09-508-832-5 Sequence 5, Application US/09508832

```
Initial Score = 300 Optimized Score = 362 Significance = 1.49
Residue Identity = 71% Matches = 422 Mismatches = 0
Gaps = 168 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
ATGCCAAGCAACCTTCTGATGTAAGTCTTCTGAGTGTGACAGAGAAGGTGACAAATTCAGACCTGCTGAGAGG
|||||
ATGCCAAGCAACCTTCTGATGTAAGTCTTCTGAGTGTGACAGAGAAGGTGACAAATTCAGACCTGCTGAGAGG
X 10 20 30 40 50 60 70
80 90 100 110 120
CTCTCCAGCTCAGGCTGGGGCCCTAGCTCCCTACAGACAGAAACCGCA-----
|||||
CTCTCCAGCTCAGGCTGGGGCCCTAGCTCCCTACAGACAGAAACCGCAAGTAAATCCCGAGCGGAAGG
80 90 100 110 120 130 140
GACCGGTGCCCCACGCGCCTCAGGGCCGCTGCGCCACCGCCAGCCCTTGCCCTTTTGTACCA
150 160 170 180 190 200 210
-----
TCCCCACTTTTTCATCTTTGTGAGAAGATCTTCTGCTGTCGCGGTCCCTCAGTGGGATTTCTCTTTGAC
220 230 240 250 260 270 280
-----
130 140 150 160 170 180 190
--AGACAGAGCGCGCACCATTGTTGTGACAAGTCAACAAACCCCAAGTCTCTCTTGGCAGGCTTC
|||||
ACAGACAGAGCGCGCACCATTGTTGTGACAAGTCAACAAACCCCAAGTCTCTCTTGGCAGGCTTC
290 300 310 320 330 340 350 360
200 210 220 230 240 250 260
AACCCTATCTCAGTCAATGGCTTCCATACGACGCTCAGGAGAACTGAAGATCTCGCGCCGAGATA
|||||
AACCCTATCTCAGTCAATGGCTTCCATACGACGCTCAGGAGAACTGAAGATCTCGCGCCGAGATA
370 380 390 400 410 420 430
```

```
270 280 290 300 310 320 330
CGGATTGCACAGAGCTCGGGCGGATCGGAGACGAGTTCAACGAACTTACACAAGGAGGTTGTTTGCAAAT
|||||
CGGATTGCACAGAGCTCGGGCGGATCGGAGACGAGTTCAACGAACTTACACAAGGAGGTTGTTTGCAAAT
440 450 460 470 480 490 500
340 350 360 370 380 390 400
GATTACCGGAGGCTGAAGACCACTCAATGTTTATCTTACAACTGTTACGCTTTATCTTCCCTCTGGTA
|||||
GATTACCGGAGGCTGAAGACCACTCAATGTTTATCTTACAACTGTTACGCTTTATCTTCCCTCTGGTA
510 520 530 540 550 560 570
410 420 X
TGGAGAAGGCATTG
|||||
TGGAGAAGGCATTG
580 590
Initial Score = 245 Optimized Score = 295 Significance = 1.10
Residue Identity = 60% Matches = 365 Mismatches = 51
Gaps = 186 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
ATGCCAAGCAACCTTCTGATGTAAGTCTTCTGAGTGTGACAGAGAAGGTGACAAATTCAGACCTGCTGAGAGG
|||||
ATGCCAAGCAACCTTCTGATGTAAGTCTTCTGAGTGTGACAGAGAAGGTGACAAATTCAGACCTGCTGAGAGG
X 10 20 30 40 50 60 70
80 90 100 110 120
CTCTCCAGCTCAGGCTGGGGCCCTAGCTCCCTACAGACAGAAACCGCA-----
|||||
CTCTCCAGCTCAGACCTGGGGCCCTAGCTCCCTACAGACAGAGCAAGGTAAATCTCTGAGGCAATCAC
80 90 100 110 120 130 140
-----
GGAGTGAAGGCGAGAGTCCCGCCACGCGCCCTCAGGGCCGCTGCGCCACCTGCCAGCCCTGGCCCT
150 160 170 180 190 200 210
-----
TTTGCTACAGATCCCGCTTTTTCATCTTTATGAGAGATCTCTCCCTGCTGCTCGATCCTCCAGTGGGTAT
220 230 240 250 260 270 280
-----
130 140 150 160 170 180
-----AGACAGAGCGCGGCGCCATGAGTGTGACAAGTCAACAAACCCCAAGTCCCTCT
|||||
TTCTCTTTTGACACAGACAGAGAGCCCGCCATGAGTGTGACAAATCAACACAAACCCCAAGTCCCTCT
290 300 310 320 330 340 350 360
190 200 210 220 230 240 250
TGCCAGGCTTCAACCACTATCTCAGTGCATGCTTCCATACGACGAGTTCAGGAGGAACCTGAAGATCTG
|||||
TGCCAGGCTTCAACCACTATCTCAGTGCATGCTTCCATGAGGAGGCT-----GAACCTGCAGATATG
370 380 390 400 410 420
260 270 280 290 300 310 320
CGCCGAGATACGAGTTCACAGAGCTGCGGCGGATCGGAGACGAGTTCAACGAACTTACACAAGGAGG
|||||
CGCCGAGATATGATCGCCCAAGAGTTCGCGGCTATCGGAGACGAGTTAACGCTTACTATGCAAGAGG
430 440 450 460 470 480 490
330 340 350 360 370 380 390
GTGTTTGCAAATGATTACCGCGGAGCTGAAGACCCCTCAATGGTATCTTACAACCTGTTACGCTTTATC
|||||
GTATTTTGAATTAATCCAAAGCAGCGCGGAGACCCACCAAGATGTTATCTTACGACTGTTACGTTACAT
500 510 520 530 540 550 560 570
```

```

5. US-09-508-832-3 (1-422)
US-09-508-832-1 Sequence 1, Application US/09508832

Initial Score = 209 Optimized Score = 398 Significance = 0.84
Residue Identity = 78% Matches = 332 Mismatches = 0
Gaps = 90 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
ATGGCCAAAGCAACCTTCTGATGTAAGTTCTTGAGTGTGACAGAGAAGGTGGACAATATGCAAGCTGCTGAGAGG
ATGCGCAAGCAACACCTTCTGATGTAAGTTCTTGAGTGTGACAGAGAAGGTGGACAATATGCAAGCTGCTGAGAGG
X 10 20 30 40 50 60 70
CTTCCCAGCTCAGGCTGGGGCCCCCTACCTCCTACAGACACAGAACGGCAAGACAGAGGCCCGCACCACTATCTCAGTGCATGGCT
CTTCCCAGCTCAGGCTGGGGCCCCCTACCTCCTACAGACACAGAACCGCAA-----
80 90 100 110 120 130 140
AGTTGTGACAAGTCAACACAAACCCCAAGTCCTCCTTGCCAGGCGCTTCAACCACTATCTCAGTGCATGGCT
-----GCT-----

220 230 240 250 260 270 280
TCCATACGACAGTCTCAGGAGGAACCTGAAGATCTGCGCCGAGATACGGATTCACAGAGACTGCGGGGG
TCCATACGACAGTCTCAGGAGGAACCTGAAGATCTGCGCCGAGATACGGATTCACAGAGACTGCGGGGG
130 140 150 160 170 180 190
290 300 310 320 330 340 350 360
ATCGGAGACAGTTCAACGAACTTACACAAGGAGGGTGTTCGAAATGATTACCGGAGGCTGAAGACAC
ATCGGAGACAGTTCAACGAACTTACACAAGGAGGGTGTTCGAAATGATTACCGGAGGCTGAAGACAC
200 210 220 230 240 250 260 270

CCTCAATGGTTATCTTACAACCTGTACGCTTTATCTTCGCTGTGGTATGGAGAAGCATTTG
CCTCAATGGTTATCTTACAACCTGTACGCTTTATCTTCGCTGTGGTATGGAGAAGCATTTG
280 290 300 310 320 330 X
370 380 390 400 410 420 X

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TGGAGAAGGCATTG
580 590

2. US-09-508-832-5 (1-590)

US-09-508-832-9 Sequence 9, Application US/09508832

Initial Score = 374 Optimized Score = 508 Significance = 1.60
Residue Identity = 86% Matches = 523 Mismatches = 61
Gaps = 18 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
ATGCCAAGCAACCTTCTGATGAAGTTCTGAGTGTGACAGAGAAGGTGACAAATTCAGCCCTGCTGAGAGG
|||||
ATGCCAAGCAACCTTCTGATGAAGTTCTGAGTGTGACAGAGAAGGTGACAAATTCAGCCCTGCTGAGAGG
X 10 20 30 40 50 60 70

CTTCCCGAGCTCAGGCTGGGGCCCTACCTCCCTACAGACAGAACCGCAAGGTAATCCCGAGGCG-----
|||||
CTTCCCGAGCTCAGGCTGGGGCCCTACCTCCCTACAGACAGAACCGCAAGGTAATCCCTGAAGGCAATCAC
80 90 100 110 120 130 140

-----GAAGGGACCGCTCCCGCCAGCGGCGCTCAGGGCCGCTGGCCCGACCGCGAGCCCTGGCCCT
|||||
GGAGGTGAAGGGACAGCTGCCCGCCAGCGGCGCTCAGGGCCGCTGGCCCGACCGCTGGCCCGCTGGCCCT
150 160 170 180 190 200 210

210 220 230 240 250 260 270
TTTGCTACAGATCCCGACCTTTTCATCTTTGTGAGAAGATCTTCTCTGTGTCCTCCGCTCCTCAGTGGGTAT
|||||
TTTGCTACAGATCCCGACCTTTTCATCTTTGTGAGAAGATCTTCTCTGTGTCCTCCCTGCTCGATCTCAGTGGGTAT
220 230 240 250 260 270 280

280 290 300 310 320 330 340
TTCTCTTTTACAGACAGACAGCGCGCGACCATGATGTTGTGACAAAGTCAACACAAACCCCAAGCTCTCT
|||||
TTCTCTTTTACAGACAGACAGCGCGCGACCATGATGTTGTGACAAAGTCAACACAAACCCCAAGCTCTCTCT
290 300 310 320 330 340 350 360

350 360 370 380 390 400 410 420
TGCAGCGCTTCAACCACTATCTCAGTGCATGGCTTCCATACGACAGTCTCAGGAGGACCTTGAAGATCTG
|||||
TGCAGCGCTTCAACCACTATCTCAGTGCATGGCTTCCATACGACAGTCTCAGGAGGACCTTGAAGATCTG
370 380 390 400 410 420

CGCCCGAGATACGGATTGCACAGGAGCTCGGGGATCGGACAGGTTCAACGAACTTACACAGAGG
|||||
CGCCCGAGATACGGATTGCACAGGAGCTCGGGGATCGGACAGGTTCAACGAACTTACACAGAGG
430 440 450 460 470 480 490

500 510 520 530 540 550 560
GTGTTTCAATGATTACCGGAGGTGAGACACCGCTCAATGGTTATCTTACAACTGTTACGCTTTATC
|||||
GTGTTTCAATGATTACCGGAGGTGAGACACCGCTCAATGGTTATCTTACAACTGTTACGCTTTATC
500 510 520 530 540 550 560 570

570 580 590
TTCCGCTGCTATGGAGAGGCATTG
|||||
GTCCGCTGCTGTTGGAGAGTGCATTG
580 590 X

3. US-09-508-832-5 (1-590)

US-09-508-832-3 Sequence 3, Application US/09508832

Initial Score = 300 Optimized Score = 362 Significance = 1.16
Residue Identity = 71% Matches = 422 Mismatches = 0
Gaps = 168 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
ATGCCAAGCAACCTTCTGATGAAGTTCTGAGTGTGACAGAGAAGGTGACAAATTCAGCCCTGCTGAGAGG
|||||
ATGCCAAGCAACCTTCTGATGAAGTTCTGAGTGTGACAGAGAAGGTGACAAATTCAGCCCTGCTGAGAGG
X 10 20 30 40 50 60 70

CTTCCCGAGCTCAGGCTGGGGCCCTACCTCCCTACAGACAGAACCGCAAGGTAATCCCGAGGCGCAAGGG
|||||
CTTCCCGAGCTCAGGCTGGGGCCCTACCTCCCTACAGACAGAACCGCA-----
80 90 100 110 120 130 140

150 160 170 180 190 200 210
GACCGCTGCCCGCCAGCGACCGCTCAGGGCCGCTGGCCCGACCGCCCTGGCCCTTTTCTGCTACACGA

220 230 240 250 260 270 280
TCCCGACCTTTTCATCTTTGTGAGAAGATCTTCTGCTGTCCTCCGCTCCTCCAGTGGGTATTTCTCTTTGAC

290 300 310 320 330 340 350 360
ACAGACAGAGCGCGCACCCATGATGTTGTGACAAGTCAACACAAACCCCAAGTCTCTTGTGCGAGGCTTC
|||||
--AGACAGAGCGCGCACCCATGATGTTGTGACAAGTCAACACAAACCCCAAGTCTCTTGTGCGAGGCTTC
130 140 150 160 170 180 190

370 380 390 400 410 420 430
AACCACATCTCAGTCAATGGCTTCCATACGACAGTCTCAGGAGAACCTGAAGATCTGCGCCCGAGATA
|||||
AACCACATCTCAGTCAATGGCTTCCATACGACAGTCTCAGGAGAACCTGAAGATCTGCGCCCGAGATA
200 210 220 230 240 250 260

440 450 460 470 480 490 500
CGGATTGCACAGAGGTGCGGGATCGGAGACGAGTTCAACGAACTTACACAGAGGAGGTGTTTGCAGAAAT
|||||
CGGATTGCACAGAGGTGCGGGATCGGAGACGAGTTCAACGAACTTACACAGAGGAGGTGTTTGCAGAAAT
270 280 290 300 310 320 330

510 520 530 540 550 560 570
GATTACCGGAGGCTGAAGACCACTCAATGGTTATCTTACAACTGTTACGCTTTATCTCCGCTCTGTA
|||||
GATTACCGGAGGCTGAAGACCACTCAATGGTTATCTTACAACTGTTACGCTTTATCTCCGCTCTGTA
340 350 360 370 380 390 400

580 590
TGGAGAAGGCATTG
|||||
TGGAGAAGGCATTG
410 420 X

4. US-09-508-832-5 (1-590)

US-09-508-832-7 Sequence 7, Application US/09508832

Initial Score = 238 Optimized Score = 299 Significance = 0.79
Residue Identity = 61% Matches = 365 Mismatches = 51
Gaps = 174 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
ATGCCAAGCAACCTTCTGATGAAGTTCTGAGTGTGACAGAGAAGGTGACAAATTCAGCCCTGCTGAGAGG
|||||
ATGCCAAGCAACCTTCTGATGAAGTTCTGAGTGTGACAGAGAAGGTGACAAATTCAGCCCTGCTGAGAGG
X 10 20 30 40 50 60 70

CTTCCCGAGCTCAGGCTGGGGCCCTACCTCCCTACAGACAGAACCGCAAGGTAATCCCGAGGCGCAAGGG
|||||
CTTCCCGAGCTCAGGCTGGGGCCCTACCTCCCTACAGACAGAACCGCA-----
80 90 100 110 120 130 140

Sequence	Initial Score	Optimized Score	Significance
US-09-508-832-5 (1-590)	209	245	Mismatches = 256
US-09-508-832-1 Sequence 1, Application US/09508832	75%	75%	Substitutions = 6
			Conservative Substitutions = 6

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410 X
TGGAGATGCATTG
|||||
TGGAGAAGGCATTG
580 590

5. US-09-508-832-7 (1-416)
US-09-508-832-1 Sequence 1, Application US/09508832
Initial Score = 151 Optimized Score = 240 Significance = 0.47
Residue Identity = 65% Matches = 272 Mismatches = 60
Gaps = 84 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
ATGCCAAGCAACCTTCTGATGTAAAGTTCTGAGTGTGACCGAGAGGTAGACAAATTCAGCCCTGCGGAGAGG
|||||
ATGCCAAGCAACCTTCTGATGTAAAGTTCTGAGTGTGACAGAGAGGTGACAAATTCAGCCCTGCTGAGAGG
X 10 20 30 40 50 60 70
80 90 100 110 120 130 140
CCTCCCGAGCTCAGAGCTGGGGCCCTTACCTCCCTACAGACAGAGCCACAGAGAGCCAGCCACCCCATG
|||||
CCTCCCGAGCTCAGAGCTGGGGCCCTTACCTCCCTACAGACAGAGCCAGAGCTTCCATACGA-----
80 90 100 110 120 130
150 160 170 180 190 200 210
AGTTGTGACAAATCAACACAAACCCCAAGTCCCTTGCCAGGCGCTTCAACCACATCTCAGTGCATGGCT

220 230 240 250 260 270 280
TCCATGAGGAGGCTGAACCTGACAGATATGCCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATCGGA
|
---CAGTCTCAGGAGGAACCTGAAGATCTGCGCCCGGAGATACGGATTGCACAGAGAGCTGCGGCGATCGGA
140 150 160 170 180 190 200
290 300 310 320 330 340 350 360
GACGAGTTTAACGCTTACTATGCAAGGAGGATTTTGAATTAATTACCAAGCAGCCGAGACCCACGCA
|||||
GACGAGTTCAACGAAACTTACAAAGGAGGATTTGCAAAATGATTACCGGAGGCTGAAGACCCCTCAA
210 220 230 240 250 260 270
370 380 390 400 410 X
ATGTTATCTTACGACTGTACGTTACGTTACATTGTCGCGCTGGTGGAGATGCATTG
|||||
ATGTTATCTTACAACTGTACGCTTATCTTCGCTGCTGGTGGAGAGGCATTG
280 290 300 310 320 330 X

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